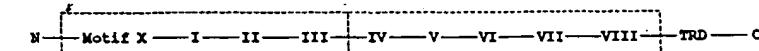
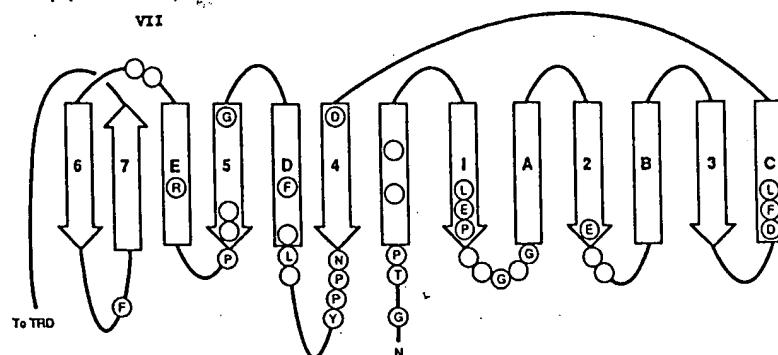


Figure 9

NEW



Group Y



Protein	Motif X		Motif I	Motif II	Motif III	
	VIII	VI			I	II
AccI (N6)	30	QDQGKfpAYayakW	55	YLERAfGIVLysrAI	77	niKAFPVD
BanIII	16	QahHmttdgdlFakrL	49	GDDscdceLlsl	69	fnnidv
BsuBI	26	QDQGKsssiFmacLF	52	YLDAGAdiesLtaF	79	dhlL
CviBIII	26	QDQGKtakrekfgFT	53	YDQGKscctceLlsc	75	sikG
Eco57I	14	QDQGKqmladyVckWV	39	YDQGKscdgvVlqAI	65	cfeL
HincII	10	QDQGKthaykYlqigM	34	YDQGKssneLdsL	55	nltsY
PaeR7I	-10	QDQGKttselvdFuldra	22	YDQGKscfGcgvVlPI	83	KreG
PstI	36	QDQGKsssaLlanLF	61	YDQGKscdgvLtaAF	110	KiRA
TaqI	19	QDQGKtVvvdFvvea	43	YDQGKAcadGpVtrAF	66	RfvC
TthHB8I	17	QDQGKtVvpgLtrFvvgta	41	YDQGKAcadGpVtrAF	64	RfvC
VspI	116	QDQGKtakkaadLfdY	141	YDQGKscctceLlsc	181	devA
EcoRI	50	PrvsnFFkYFavnFdnL	79	nkEGFssseaaknGF	104	KlvfdDIS
COMtase	41	nvgdakqqIMdaVIreY	62	VLELGaycGysavrM	85	RlltMEMN
HhaI (C5)	298	GNSVvinVlqyIaynIg	14	WIDLFaGlgFrlAL	35	cvysNEWD

Protein	Motif IV		Motif V	Motif VI	Motif VII	
	—4—	—5—			—E—	—D—
AccI (N6)	117	QDQGKtNPFkFkhdyn	154	MDt1E1LksL-hQsQnrcaxVlls	190	WtqydksktLrhk
BanIII	132	VQ1tBtNPFkFkhdyn	166	DQGhdkava-ttQdLsVtqVlq	202	Wqfiaenydnie
BsuBI	137	QDQGKtNPFkFkiksnsK	168	MDt1E1LksL-dlMSGcgvVlPI	204	FqghdlnktsLkhk
CviBIII	113	QDQGKtNPFkFvrrpsgyK	141	MDt1E1LksL-kcbehkredolap	178	WvLkltldiLsfe
Eco57I	110	QDQGKtNPFkFvqfleR	149	MDt1E1LksL-allLqGdLqMVl	185	Dsylqghvcsvkiv
HincII	85	QDQGKtNPFkFwknlse	123	MDt1E1LksL-lqLqVcGelLqdy	159	DnkfLinnngsPek
PaeR7I	114	QDQGKtNPFkFwknlse	149	MDt1E1LksL-lqLqVcGelLqdy	185	LksLvaerfhLkvY
PstI	146	QDQGKtNPFkFwknlse	177	MDt1E1LksL-kqLqVcGelVat	213	FrkqkLdecslmkh
TaqI	99	QDQGKtNPFkFgivgeasK	141	MDt1E1LksL-rLqLqVcGelVat	177	LeffLaregktsvYY
TthHB8I	97	QDQGKtNPFkFgivgeasK	139	MDt1E1LksL-rLqLqVcGelVat	175	LeffLaregktsvYY
VspI	211	QDQGKtNPFkFgivgeasK	265	MDt1E1LksL-rLqLqVcGelVat	310	Wkqcpddqhatic
EcoRI	133	sDiVvtNPFfslfreyld	175	MDt1E1LksL-rLqLqVcGelVat	208	aRidsngnriIspnn
COMtase	135	1DmVf1Dhwk-----	147	MDt1E1LksL-rLqLqVcGelVat	183	VRgsssfecthYssYL
HhaI (C5)	72	hDlCagfPCQAfisgk	99	MDt1E1LksL-rLqLqVcGelVat	136	VKnMn1DysFhakV

Protein	Motif VIII	MW	Target	Swissprot	
				Accession Number	
AccI (N6)	209 eenWddal	540 aa	GTMKAC	P25201	
BanIII	220 dtkLsaav	580 aa	ATCGAT	P22772	
BsuBI	223 rdkakGkde	501 aa	CTCGAG	P33563	
CviBIII	194 dkhdcdt	377 aa	TCGA	P10835	
Eco57I	202 keiWpedtl	540 aa	CTCGAG	P25240	
HincII	177 eskVhgv	502 aa	GTYRAC	P17744	
PaeR7I	203 dtpaFhsdv	531 aa	CTCGAC	P05103	
PstI	232 rksaFksad	507 aa	CTCGAG	P00474	
TaqI	192 lgeVpgrkk	421 aa	TCGA	P14385	
TthHB8I	190 lgeVpgrkk	428 aa	TCGA	P25749	
VspI	333 sqrmeknp	408 aa	ATTAAT	Q03055	
EcoRI	228 nldVfirhk	325 aa	GAATTC	P00472	
COMtase					
HhaI (C5)	161 QkReRiymi	221 aa	catechol	P22734	
		327 aa	GCGC	P05102	

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		NXXXXXXXLXELVXKYEXXRSTXLXSTYNETXLRS					
BpmIRM		10	20	30	40		
AcuIRM		- - - - M	H I S E L V D K Y K A H R S T F L K P T Y N E T Q L R N D			30	
BsgIRM		- - - - M	V H D H K L E L A K L I R N Y E T N R K E C L N S R Y N E T L L R S D			36	
ThaRM		- - - - M	N R V E S K K K L E Q L V Q Q F E K Y E S T Y S A S D Y K E A T L R S S			37	
		MSNENYNI	D F E R V K E L I L K Y E Q V K K S G E I K T Y N E E S T K K D			40	
		FLDPLFELLGWDXXNXXGTNXXXREVI XEELEX - - EEXX					
BpmIRM		50	60	70	80		
AcuIRM		F I D P L L K S L G W D V D N T K G K T H I L R D V I Q E E Y I E I K D E E T K				70	
BsgIRM		Y L D P F F E L L G W D I K N K A G K P T N E R E V V L E E A L K A S A S E H S				76	
ThaRM		F L D P F F E L F G W E M R P E R I T N P A D L E V I I E E S L E T - - E K S T				75	
		F I E P L F K S L G W N F S N R G K T N D S - - - V S A E E T I S K - - - - -				72	
		KXPDYTFRI NGTRKFFVEAKKP- SENI X K X X K X A F Q A R R Y					
BpmIRM		90	100	110	120		
AcuIRM		K N P D Y T L R I N G T R K L F V E V K K P - S F N I L K S A K A A F Q T R R Y				109	
BsgIRM		K K P D Y T F R L F S E R K F F L E A K K P - S V H I E S D N E T A K Q V R R Y				115	
ThaRM		K Y I D Y V F K I N R T T Q F L V E A K K P - A E S L S K - K D H I F Q A K S Y				113	
		K R V D Y G F R I N G I P K F F L E A K P L R E E N I Q N N S K Y V T Q A I D Y				111	
		GFTAXLXI SVLTNFEXLVI YDXSXKPDXD- XXXKARXKX					
BpmIRM		130	140	150	160		
AcuIRM		G W S A N L G I S V L T N F E H L V I Y D C R Y T P D K S D - N E H I A R Y K V				148	
BsgIRM		G F T A K L K I S V L S N F E Y L V I Y D T S V K V D G D D - T F N K A R I K K				154	
ThaRM		A F T T E I P F V I L T N F K E F R F Y D V S T E P L H N Q P D T D K V E E Y C				153	
		A W M K S C S W A I L T N F E T V A V Y N A D W K E S N Y G - - - - S - N L L				145	
		FXYXEYEXXFDEI XDLLSREAVXSGXLDKXXXK- - - - -					
BpmIRM		170	180	190	200		
AcuIRM		F S Y E E Y E E A F D E I K D I I S Y E S A N S G A L D E M F D - - - - -				181	
BsgIRM		Y H Y T E Y E T H F D E I C D L L G R E S V Y S G N F D K E W L S - - - - -				188	
ThaRM		F D Y K E Y V Q N F D K L W E L F S R E A V A N R S L A K F Y A K R R N I V D S				193	
		F I L H P N D F L T D E R F K Y L S K K A F E N G E L D K I A S K - - - - -				179	
		YXNKXXXXXXDXFLQQI XXWREXLAXEI XKN					
BpmIRM		210	220	230	240		
AcuIRM		- - - - - V N T R V G E T F D E Y F L Q Q I E N W R E K L A K T A I K N				211	
BsgIRM		- - - - - I E N K I N H F S V D T L F L K Q I N T W R L L L G E E I Y K Y				219	
ThaRM		P D L I F K L N Y Q I D K G A S L L D I S F L K N L K I W R K S L A E N I F N N				233	
		- - - - - Y G K K Q L K N P I D K Q L L Q D M I H F R E V L S K D I V K N				210	
		NX - - X L X E N E V N E I V Q R I L D R L I F L R V C E D R N L E X Y E T L K					
BpmIRM		250	260	270	280		
AcuIRM		N T - - E L G E E D V N F I V Q R L L N R I I F L R V C E D R T I E K Y E T I K				249	
BsgIRM		Q P - - T I Q E N E L N D I V Q S Y L N R I I F L R V C E D R N L E T Y Q T L L				257	
ThaRM		N - - S L N V N V I N E V V Q R I L D R L I F I R I I E D R N I E S K E F L K				270	
		N Q D K H L T Q D E V D E S V Q R I L D R L I F I R N A E D R G L E E N Q L Q S				250	

Figure 10-1

	XI XXXXE-----	XXELXDLFKXXDRKFNSGLFDFXDHT	
	290	300	310
BpmIRM	SI KN-----	YEELKDLFQKSDRKFNNSGLFDFIDDT	279
AcuIRM	NFASSND-----	FSALIDKFKQADRCYNSGLFDQLLTE	290
BsgIRM	EIVEMHEQDNSI	SVKNELDKLCIELNKKFNG--LVFHDHT	308
ThaRM	ILRQWYEKGKG-	HLMKEISRIYKDFDDKYNS---KLFAHH	286
	LXXEXXI DNEVLI VI XXLYYPKSP---	YDFSVIXSDIL LG	
	330	340	350
BpmIRM	LLLEVEI DSNVLI EI	FSDLYFPQSP---YDFSVVDPTILS	316
AcuIRM	QIIEEDISS--VFWVI	I KQLYYPESP---YSFSVFSSDL LG	325
BsgIRM	FVNEALI DNEI LI VI	I DNLYYPKSP---YNFRLIKPEIL LG	345
ThaRM	LCDDL YI DNEALQEVI	EGLNHSKDDSYRYDFSVIESDVLG	326
	NI YEXFLGEKI XI EXGKTXLXXXNXXX--	GVVYTPSYI	
	370	380	390
BpmIRM	QI YERFLGQEII	ESGGTFHI TESPEVAASN	356
AcuIRM	NI YEI FLSEKLVI	NQSRVELVKKPENLDR--	363
BsgIRM	RI FEQFLGEKI EII	DGKITLGLKDI NKKSG-	384
ThaRM	NI LKSTP-	KRAKLEESKTHRKEQ-----	357 (Mutif)
	GVVPTPKII		
	400		
	VEXI VKNTVXPKXX-	GKTXEELXQLKI ADI ACGSGSFLIS	
	410	420	430
BpmIRM	VEQIVKDTLTPLTE-	GKKFNELCNLKI ADI CCGSGTFLIS	395
AcuIRM	I NDI LRNTVLPKCY-	GKTDIELQLKFADI ACGSGAFLLE	402
BsgIRM	VEKI VENTLSKKLHNDI	TI ENLEQIKI ADI ACGSGSFLIS	424
ThaRM	VDYIVKNTVGEYIK-	THTPEEIKKVRI LDPAACGSGSFLIR	396
	440		
	SYKXLXDKXXXXYXXXXXDDSQ-----	LVXXXXGXLXLT	
	450	460	470
BpmIRM	SYDFLVEKVMEKII	EENI DDSD-----LVYETEEGLIL	429
AcuIRM	LFQLLNDTLVDYLLSS--	DTSQ-----LIPTGI GTYKLS	434
BsgIRM	SYKYLI DKFQYI	YSKCSEADVQTLISNNLVFI DNGKLMLT	464
ThaRM	AYKELENYWKQNSDFAQLTLD	S-----EEF	421
	480		
	SYEXKRXI LXNNI FGVDXDPXAVEVAKL	SLLLKLEGE--X	
	490	500	510
BpmIRM	LKAKRNI LENNL	FGVDVN PYAVEVAEFSLLL	469
AcuIRM	YEI KRKVLLSCI	NAVAAFKGLLL	474
BsgIRM	MEHKKGI LQONI	KLLEGEDVQ	502
ThaRM	YSKKVEILRNNI	YGVLDLDPKAVEIAQLNLLQI LEKK--	459
	520		
	SXXNXR-----	PI LPDLXDNIXXGNSLXDN-----PEXL	
	530	540	550
BpmIRM	SVNNFI HEHEDKI	LPDLTSII KCGNSLVDNKFFEFMPESL	509
AcuIRM	SI ANI R-----	PVLPDLLDNILFGNSLLE-----PEKV	502
BsgIRM	REGTLR-----	PI LPDLNDNI KHGNSSIDN-----EIL	530
ThaRM	-----	QRLPLLQNNIKVGNS-----L	474
	560		

Figure 10-2

	EDDXI	XXDXNX	-	-	FEWE	-	-	FPDI	MXNGGF	DV	I	GNPP	YV			
BpmIRM	EDDE	I	570	LFKANP	-	-	FEWEE	FPDI	MANGGF	DAI	I	GNPP	YV			
AcuIRM	ELD-	HQVEVN	-	-	-	-	-	PLDFSDL	KFDV	I	VGNPP	Y				
BsgIRM	FEDD	I	580	NYDI	DATL	PFDWE	YAPPDI	I	DNGGF	DV	I	LGNPP	Y			
ThaRM	I	DDPSI	590	SDRAFK	WEEE	-	-	FPEI	MKI	GGFDTI	I	GNPP	YV			
	RI	QNMKXXX	XPX	EXXXY	XKK	-	-	YXVAAK	KNFDI	YFLF	I	EK				
BpmIRM	RI	QNMKKY	SPEE	I	EYYQSKD	SEYTVAK	KETV	DKYFL	FI	ER						
AcuIRM	KSEDMKNI	TPLEL	PLYKKN	-	-	-	-	DKYFL	FL	LER						
BsgIRM	RI	QI	FEEL	YGKD	VVNYL	KK	-	KYVSAEK	FNF	DI	YVVFI	EK				
ThaRM	RI	QNL	NDE	-	-	-	-	FKSAYK	NY	DI	YLLF	VEK				
	ALXLL	NEXGI	LGYI	VPSKFF	XTXYGKKL	RELI	TEKKXL	YK								
BpmIRM	ALI	LLNPT	GLL	GYI	I	PHKFF	I	TKGGKE	L	RKF	I	AEKHQI				
AcuIRM	GLALL	KEEGI	L	GYI	VPSKFT	KVGAGKKL	RELL	TDKGY	L	DS						
BsgIRM	ALSLL	NDQGI	L	GYI	VMNKFF	TTQYGEKL	RELI	TSQKLL	YE							
ThaRM	SFDL	CKENG	I	GFII	I	PSKFI	NAYYGL	GLRNLI	SETKSL	YK						
	Box G (Motif II)															
	Box H (Motif VII)															
	I	I	DFGXNQI	FXDAAT	YTCI	L	I	LXKT	XDXF	KYXXV	XNL	XT				
BpmIRM	I	I	690	NFGVTQVF	PGRATYT	A	I	L	I	QANKMAQF	KYKKVSNI	SA				
AcuIRM	I	VSGANQI	FQDKTT	YT	CLLI	L	RKTPHTDF	KYAEVRNL	I	D						
BsgIRM	I	I	DFFGI	NEI	FNNATT	YT	CI	L	LDKTNPDE	III	ERVI	DLNT				
ThaRM	LI	DFKD	VQI	FGDA	ANYT	CI	LFLKI	YKNDVFSYI	FPKSTD	T						
	Box I (Motif I)															
	WTXXSXS	NXXVXS	-	-	XXLX	-	-	SDPWI	LSSNEXEE	VYXKF						
BpmIRM	ETLDSE	ENTCVYSS	-	-	EKYN	-	-	SDPWI	FLSPETE	AVFTKF						
AcuIRM	WKVRKA	DAMEF	SQQQL	STLQ	-	-	-	SDAWI	L	I	PSEL	ISVYHQI				
BsgIRM	WKAGE	ESSDR	KVVDH	-	TEFT	-	-	STPWYL	SSNTDEE	I	YKFF					
ThaRM	FTI	QSVSNV	DTFQEYKL	PLPKPD	HFWI	-	-	LSENKV	SELEI	RKL						
	Box II (Motif II)															
	X	EXXX	LEXI	S	-	I	DNI	FVGL	QTSAD	XVYI	FXPE	ETXD	Y			
BpmIRM	TEA	-	QFEKL	GEI	TDI	S	VGL	QTSAD	KI	YI	FI	PENET	SDTY			
AcuIRM	LAQSQ	KLE	DI	VGI	DNI	F	NGI	QTSAND	VYI	F	VPT	HED	TENY			
BsgIRM	EENMV	LLET	I	S	-	DRV	FVG	VQTDCDP	VYI	LEEVYEE	ENYL					
ThaRM	SRKG	I	PLE	I	S	-	KNI	FQSL	TTSA	DGI	YFVQ	VESET	RTDA			
	Box III (Motif III)															
	YFX	-	KKG	XEY	KI	E	KX	I	L	KPXL	KGXS	-	-	I	XXYXXXXX	N
BpmIRM	I	FN	-	YKGK	RYEI	E	KSI	CCPAI	YDLS	-	-	FGSF	E	I	QGN	
AcuIRM	YFI	-	KKG	QEY	KI	E	KEI	TKPYF	KTTSG	GED	NLYTYRT	FKPN				
BsgIRM	YCK	SEY	TT	EVHK	FEKD	DHL	KPFL	KGS	LD	-	-	I	KKY	TFS	NVN	
ThaRM	KI	RNI	KNN	LEFA	VEKT	I	LRK	LLKG	KD	-	-	I	RRCS	VDW	WKG	

Figure 10-3

<u>AXVI F PYTXXDXAXLI PLXTI KXXFPLAYKYLXSXKEXL</u>			
BpmIRM	850	860	870
AcuIRM	AQMI F PYE I RDEEAYL LEEETLENDYPLAWNLYLNEFKEAL		880
BsgIRM	ARVI Y PYTQTESSVELI PLDEI REI F PLAYKYLMSLKFL		814
ThaRM	KWLL F PYTNSENTSDLI PETTYKQYFPETWKYLESCKERL		802
	SYVVYPYLVKDDKASLI TLSEI KDRYPLAYEYFKHYELQL		839
			777
<u>XX- KRSI XXR- - - - XNEWHQYGRXQSLXKFX- QXKI VX</u>			
BpmIRM	890	900	910
AcuIRM	E- - KRSLQGR- - - - NPKWYQYGRSQSLSKFHDKEKLI W		920
BsgIRM	SSPKRDI KPRPKT- - - TNEWHRYGRHQSLDNCGLSQKII V		839
ThaRM	AK- RKSIERELDI NPNEYNEWYKYI YKKNHTRMD- QLKI VF		877
	KTREDNKLKD- - - - DENWHQYI YRKNLEKFE- QKKI VT		810
<u>XVLAXGXXFAI DXNG- - - FLFSGGNGGGXXI VLPDQSXY</u>			
BpmIRM	930	940	950
AcuIRM	TVLATKPPYVLDRNN- - - LLFTGGGNG- - PYYGLI NQSI Y		960
BsgIRM	GVLSVGDKYAI DTYG- - - TLISSGGTAGYCVVALPDDCKY		881
ThaRM	PAI SKGSSFCYDSDGEYYFVGSGAGGGGGGAI VL PDDCKY		876
	QVLASKNTFAIDLNG- - EFYFVGGDNAGGYGI VL NDNNQN		917
			848
<u>SYYYLLGI LNSXVLEXXXKXRGSXFRGGYYSXGKKFI ENL</u>			
BpmIRM	970	980	990
AcuIRM	SLHYFLGI LSHPVI ESMVKARASEFRGSYYSHGKQFI EKI		1000
BsgIRM	SIYYLQAI LNSKYLEWFSALHGEVFRGGYI ARGTVLKNL		921
ThaRM	NYLSLLGI LNSEVVSYQI VRRGSKHKGSYYGVDKKRI ENL		916
	MYYFVLALLNSNVLEFYLKNI STPFRGGYFSYKRFIDKL		957
			888
<u>PI RKI DFDNX- E- NLFDXVSTXVKELIXIXDKI XXXXNTD</u>			
BpmIRM	1010	1020	1030
AcuIRM	PI RKI DFDQDEVVKYNTVVTVEKLI ITTDRI KSESNGP		1040
BsgIRM	PI RKI DFDNLEEANLHDLIATKQKELIEIYDKIDVN VNNK		961
ThaRM	YVPLI NEDNK- - - NLFSNI SKMVAQI LDAFQKMHQAGTTD		956
	PLLI PKD- - - - SRFDSVSSLSKEQMNI SKKMRNFPNTD		994
			922
<u>RRX- XLQRRDXLXXXLNQLIYELYNLXVEEXTXXXNXLX</u>			
BpmIRM	1050	1060	1070
AcuIRM	RRR- ML RRRLDALSNQLI QVI NELYNI SDEEYTTVLNDEM		1080
BsgIRM	RVL TPL QRMFKREKEVL DQLLSRLYNLGVDDSLIPYIKDL		1000
ThaRM	VGKEQL QQRI KMLNARI NELVYRLYNLPVEYKEYIKNALE		996
	ERD- LLEREYDKRCQELNQMI YEI YGLNKLEITLLDDRLC		1034
			961
<u>X- A- - - -</u>			
BpmIRM	LTAAL GEEK		1009
AcuIRM	YEAH		1000
BsgIRM	N		1035
ThaRM	Q		962

Figure 10-4